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## RAW SEQUENCE LISTING

DATE: 09/18/2002

PATENT APPLICATION: US/09/878,781

TIME: 09:57:58

Input Set : A:\seqlist.txt

Output Set: N:\CRF4\09182002\I878781.raw

ENTERED

3 <110> APPLICANT: Bolton, Alexandra J.  
4 Perez-Casal, Jose  
5 Fontaine, Michael  
6 Potter, Andrew A.  
8 <120> TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST  
9 STREPTOCOCCUS INFECTION  
11 <130> FILE REFERENCE: 9000-0055  
13 <140> CURRENT APPLICATION NUMBER: 09/878,781  
C--> 14 <141> CURRENT FILING DATE: 2002-09-10  
16 <160> NUMBER OF SEQ ID NOS: 18  
18 <170> SOFTWARE: PatentIn Ver. 2.0  
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50 <221> NAME/KEY: CDS  
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57 1 5 10 15  
59 gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc 96  
60 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile  
61 20 25 30  
63 aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tac gat 144  
64 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp

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67 aca act caa gga cgt ttt gac gga act gtt gaa gtt aaa gaa ggt gga 192
68 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
69          50          55          60
71 ttt gaa gta aac gga aac ttc atc aaa gtt tct gct gaa cgt gat cca 240
72 Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro
73 65          70          75          80
75 gaa aac atc gac tgg gca act gac ggt gtt gaa atc gtt ctg gaa gca 288
76 Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
77          85          90          95
79 act ggt ttc ttt gct aaa aaa gaa gct gct gaa aaa cac tta cat gct 336
80 Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
81          100          105          110
83 aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt 384
84 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
85          115          120          125
87 aaa aca gtt gtt ttc aac act aac cac gac att ctt gac ggt act gaa 432
88 Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
89          130          135          140
91 aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cct atg 480
92 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
93 145          150          155          160
95 gct aaa gct ctt cac gat gca ttt ggt atc caa aaa ggt ctt atg act 528
96 Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
97          165          170          175
99 aca atc cac gct tat act ggt gac caa atg atc ctt gac gga cca cac 576
100 Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
101          180          185          190
103 cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gct gca aac att gtt 624
104 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
105          195          200          205
107 cct aac tca act ggt gct gct aaa gct atc ggt ctt gtt atc cca gaa 672
108 Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
109          210          215          220
111 ttg aat ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act 720
112 Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
113 225          230          235          240
115 gga tca gta act gag ttg gtt gta act ctt gat aaa aac gtt tct gtt 768
116 Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
117          245          250          255
119 gac gaa atc aac gct gct atg aaa gct gct tca aac gac agt ttc ggt 816
120 Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
121          260          265          270
123 tac act gaa gat cca att gtt tct tca gat atc gta ggc gtg tca tac 864
124 Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
125          275          280          285
127 ggt tca ttg ttt gac gca act caa act aaa gtt atg gaa gtt gac gga 912
128 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
129          290          295          300

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131 tca caa ttg gtt aaa gtt gta tca tgg tat gac aat gaa atg tct tac 960
132 Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
133 305 310 315 320
135 act gct caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa 1008
136 Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
137 325 330 335
139 taa 1011
143 <210> SEQ ID NO: 4
144 <211> LENGTH: 336
145 <212> TYPE: PRT
146 <213> ORGANISM: Streptococcus dysgalactiae
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152 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
153 20 25 30
155 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
156 35 40 45
158 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
159 50 55 60
161 Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro
162 65 70 75 80
164 Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
165 85 90 95
167 Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
168 100 105 110
170 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
171 115 120 125
173 Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
174 130 135 140
176 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
177 145 150 155 160
179 Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
180 165 170 175
182 Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
183 180 185 190
185 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
186 195 200 205
188 Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
189 210 215 220
191 Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
192 225 230 235 240
194 Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
195 245 250 255
197 Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
198 260 265 270
200 Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
201 275 280 285
203 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly

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204      290      295      300
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213 <210> SEQ ID NO: 5
214 <211> LENGTH: 1011
215 <212> TYPE: DNA
216 <213> ORGANISM: Streptococcus agalactiae
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (1)..(1011)
222 <400> SEQUENCE: 5
223 atg gta gtt aaa gtt ggt att aac ggt ttc ggt cgt atc ggt cgt ctt 48
224 Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
225 1 5 10 15
227 gca ttc cgt cgc atc caa aac gta gaa ggt gtt gaa gtt act cgt atc 96
228 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
229 20 25 30
231 aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tat gac 144
232 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
233 35 40 45
235 aca act caa ggt cgt ttc gac ggt act gtt gaa gtt aaa gaa ggt gga 192
236 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
237 50 55 60
239 ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca 240
240 Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
241 65 70 75 80
243 gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca 288
244 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
245 85 90 95
247 act ggt ttc ttt gca tca aaa gaa aaa gct gga caa cac atc cat gaa 336
248 Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu
249 100 105 110
251 aat ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt 384
252 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
253 115 120 125
255 aaa aca gtt gtt ttc aac act aac cac gat atc ctt gat gga act gaa 432
256 Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
257 130 135 140
259 aca gtt atc tca ggt gct tca tgt act aca aac tgt ctt gct cca atg 480
260 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
261 145 150 155 160
263 gct aaa gct tta caa gac aac ttt ggt gtt aaa caa ggt ttg atg act 528
264 Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
265 165 170 175
267 act atc cac gca tac act ggt gac caa atg atc ctt gac gga cca cac 576
268 Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
269 180 185 190

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271 cgt ggt ggt gac ctt cgt cgt gct cgt gca ggt gct gca aac atc gtt 624
272 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
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275 cct aac tca act ggt gct gca aaa gct atc gga ctt gtt atc cca gaa 672
276 Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
277      210      215      220
279 ttg aac ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act 720
280 Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
281 225      230      235      240
283 gga tca gta act gaa ttg gtt gca act ctt gaa aaa gac gta act gtc 768
284 Gly Ser Val Thr Glu Leu Val Ala Thr Leu Glu Lys Asp Val Thr Val
285      245      250      255
287 gaa gaa gta aat gca gct atg aaa gca gca gct aac gat tca tac ggt 816
288 Glu Glu Val Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
289      260      265      270
291 tat act gaa gat cca atc gta tca tct gat atc gtt ggt att tca tac 864
292 Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr
293      275      280      285
295 ggt tca ttg ttt gat gct act caa act aaa gtt caa act gtt gac ggt 912
296 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
297      290      295      300
299 aac caa ttg gtt aaa gtt gtt tca tgg tac gat aac gaa atg tca tac 960
300 Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
301 305      310      315      320
303 act tca caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa 1008
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305      325      330      335
307 taa 1011
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312 <211> LENGTH: 336
313 <212> TYPE: PRT
314 <213> ORGANISM: Streptococcus agalactiae
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321      20      25      30
323 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
324      35      40      45
326 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
327 50      55      60
329 Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
330 65      70      75      80
332 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
333      85      90      95
335 Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu
336      100      105      110
338 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
339      115      120      125

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VERIFICATION SUMMARY

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TIME: 09:57:59

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date